PALM INTRANET

Day : Saturday
Date: 11/4/2006
Time: 11:35:33

Inventor Name Search Result

Your Search was:

Last Name = HEMBROUGH
First Name = TODD

Application#	Patent#	Status	Date Filed	Title	Inventor Name
10086176	6946439	150	02/28/2002	COMPOSITIONS AND METHODS FOR INHIBITING CELLULAR PROLIFERATION COMPRISING TFPI FRAGMENTS	HEMBROUGH, TODD
10608886	Not Issued	41	06/26/2003	Compositions and methods comprising protein activated receptor antagonists	HEMBROUGH, TODD
10833252	Not Issued	71	04/27/2004	Compositions and methods comprising protein activated receptor antagonists	HEMBROUGH, TODD
11183555	Not Issued	30	07/18/2005	Compositions and methods for inhibiting cellular proliferation comprising TFPI fragments	HEMBROUGH, TODD
60391655	Not Issued	159	06/26/2002	Compositions and methods of use of ligands that bind components of the blood coagulation/clotting pathway for the treatment of cancer and angiogenic-based disease	HEMBROUGH, TODD
60398662	Not Issued	159	07/26/2002	Inhibition of proteinase activated receptor-2 signalling by a peptide antagonist	HEMBROUGH, TODD
60458095	Not Issued	159	03/27/2003	Compositions and methods of use of ligands that bind components of the blood coagulation/clotting pathway for the treatment of cancer and angiogenic-based disease	HEMBROUGH, TODD
60466296	Not Issued	159	04/29/2003	Compositions and methods of use of ligands that bind components of the blood coagulation/clotting pathway for the treatment of cancer and angiogenic-based disease	HEMBROUGH, TODD
60603462	Not Issued	160	08/20/2004	Compositions and methods for inhibiting cellular proliferation comprising TFPI fragments	HEMBROUGH, TODD

09905033	Not Issued	161	07/12/2001	Inhibition of tumor growth by a nematode anticoagulant protein	HEMBROUGH, TODD A.
10612617	Not Issued	160	07/02/2003	Inhibition of tumor growth by a nematode anticoagulant protein	HEMBROUGH, TODD A.
11208460	Not Issued	25	08/19/2005	Compositions and methods comprising proteinase activated receptor antagonists	HEMBROUGH, TODD A.
60217795	Not Issued	159	07/12/2000	Inhibition of tumor growth by the nematode anticoagulant protein rNAPc2	HEMBROUGH, TODD A.
60644710	Not Issued	159	01/18/2005	Compositions and methods comprising proteinase activated receptor antagonists	HEMBROUGH, TODD A.
60749276	Not Issued	20	12/09/2005	Compositions and methods for inhibiting cellular proliferation	HEMBROUGH, TODD A.
60753363	Not Issued	20	12/22/2005	Compositions and methods comprising proteinase activated receptor antagonists	HEMBROUGH, TODD A.
60853273	Not Issued	20	10/20/2006	Compositions and methods comprising extracellular loop antibodies to proteinase activated receptors and other G-protein coupled receptors	HEMBROUGH, TODD A.

Inventor Search Completed: No Records to Display.

Search Another: Inventor **Last Name** HEMBROUGH **First Name** TODD Search

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PALM INTRANET

Day : Saturday
Date: 11/4/2006
Time: 11:35:50

Inventor Name Search Result

Your Search was:

Last Name = PRIBLUDA
First Name = VICTOR

Application#	Patent#	Status	Date Filed	Title	Inventor Name
09641327	Not Issued	161	08/18/2000	Antiangiogenic agents	PRIBLUDA, VICTOR
09779331	6995278	150	02/08/2001	ANTIANGIOGENIC AGENTS	PRIBLUDA, VICTOR
10003461	Not Issued	160	11/30/2001	Synthesis of 3-amino-thalidomide and its enantiomers	PRIBLUDA, VICTOR
10213294	Not Issued	95	08/06/2002	USE OF NITROGEN SUBSTITUTED THALIDOMIDE ANALOGS FOR THE TREATMENT OF MACULAR DEGENERATION	PRIBLUDA, VICTOR
10608886	Not Issued	41	06/26/2003	Compositions and methods comprising protein activated receptor antagonists	PRIBLUDA, VICTOR
10833252	Not Issued	71	04/27/2004	Compositions and methods comprising protein activated receptor antagonists	PRIBLUDA, VICTOR
11347880	Not Issued	30	02/06/2006	Antiangiogenic agents	PRIBLUDA, VICTOR
11513291	Not Issued	19	08/29/2006	Synthesis and anti-tumor activity of nitrogen substituted thalidomide analogs	PRIBLUDA, VICTOR
60391655	Not Issued	159	06/26/2002	Compositions and methods of use of ligands that bind components of the blood coagulation/clotting pathway for the treatment of cancer and angiogenic-based disease	PRIBLUDA, VICTOR
60398662	Not Issued	159	07/26/2002	Inhibition of proteinase activated receptor-2 signalling by a peptide antagonist	PRIBLUDA, VICTOR
10086176	6946439	150	02/28/2002	COMPOSITIONS AND METHODS FOR INHIBITING CELLULAR PROLIFERATION COMPRISING TFPI FRAGMENTS	PRIBLUDA, VICTOR P.

11183555	Not Issued	30	07/18/2005	Compositions and methods for inhibiting cellular proliferation comprising TFPI fragments	PRIBLUDA, VICTOR P.
09933894	Not Issued	160	08/21/2001	Antiangiogenic agents	PRIBLUDA, VICTOR S.
09939208	7135581	150	08/24/2001	ANTIANGIOGENIC AGENTS	PRIBLUDA, VICTOR S.
10354921	Not Issued	161	01/30/2003	Non-steroidal analogs of 2-methoxyestradiol	PRIBLUDA, VICTOR S.
10354927	Not Issued	161	01/30/2003	Non-steroidal analogs of 2-methoxyestradiol	PRIBLUDA, VICTOR S.
10375890	Not Issued	160	02/27/2003	Methods of using antiangiogenic agents	PRIBLUDA, VICTOR S.
10856340	Not Issued	71	05/28/2004	Antiangiogenic agents	PRIBLUDA, VICTOR S.
11118852	Not Issued	30	04/29/2005	Antiangiogenic agents	PRIBLUDA, VICTOR S.
11519570	Not Issued	20	09/12/2006	Methods of treating disease states using antiangiogenic agents	PRIBLUDA, VICTOR S.
60250219	Not Issued	159	11/30/2000	Synthesis of 3-aminothalidomide and its enantiomers	PRIBLUDA, VICTOR S.
60255302	Not Issued	159	12/13/2000	Antiangiogenic agents	PRIBLUDA, VICTOR S.
60278250	Not Issued	159	03/23/2001	Antiangiogenic agents	PRIBLUDA, VICTOR S.
60354046	Not Issued	159	01/30/2002	Non-steroidal analogs of 2-methoxyestradiol	PRIBLUDA, VICTOR S.
60361267	Not Issued	159	03/01/2002	New methods of using antiangiogenic agents	PRIBLUDA, VICTOR S.
60474288	Not Issued	159	05/28/2003	Antiangiogenic agents	PRIBLUDA, VICTOR S.
60492776	Not Issued	159	08/04/2003	Reformulated panzemR (2-Methoxyestradiol) shows enhanced oral bioavailability	PRIBLUDA, VICTOR S.
60552692	Not Issued	159	03/12/2004	Structure-activity relationships of new chemical entities based on the anti-tumor and anti-angiogenic agent 2-methoxyestradiol	PRIBLUDA, VICTOR S.

Inventor Search Completed: No Records to Display.

Search Another: Inventor **Last Name** PRIBLUDA **First Name** VICTOR Search

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NEWS 9	SEP 25	CAS REGISTRY(SM) no longer includes Concord 3D coordinates
NEWS 10	SEP 25	CAS REGISTRY(SM) updated with amino acid codes for pyrrolysine
NEWS 11	SEP 28	CEABA-VTB classification code fields reloaded with new classification scheme
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DICTIONARY FILE UPDATES: 3 NOV 2006 HIGHEST RN 912441-38-4

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L2 251765 GKR/SQSP
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3 GKR/SQEP
2520 SQL=3

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L3            3 GKR/SQEP
                (GKR/SQEP AND SQL=3)

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                                                       ENTRY    SESSION
FULL ESTIMATED COST                                     9.25       9.67

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=> L3
L4            4 L3

=> d 1-4 ibib abs hitstr

L4   ANSWER 1 OF 4  HCAPLUS  COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER:         1998:766878  HCAPLUS
DOCUMENT NUMBER:          130:152488
TITLE:                    Synthesis and structure-function study about tenecin
                          1, an antibacterial protein from larvae of Tenebrio
                          molitor
AUTHOR(S):                Lee, Keun Hyeung; Hong, Sung Yu; Oh, Jong Eun
CORPORATE SOURCE:         Protein Chemistry Laboratory, Mogam Biotechnology
                          Research Institute, Yongin-City, Kyunggi-Do, 449-910,
                          S. Korea
SOURCE:                   FEBS Letters (1998), 439(1,2), 41-45
                          CODEN: FEBLAL; ISSN: 0014-5793
PUBLISHER:                Elsevier Science B.V.
DOCUMENT TYPE:            Journal
LANGUAGE:                 English
AB   Tenecin 1, an inducible antibacterial protein secreted in the larvae of
     Tenebrio molitor, has a long N-terminal loop and common structural feature
     of insect defensin family corresponding to cysteine stabilized
     α/β motif.  To study the function of the N-terminal loop and
     disulfide bridges, N-terminal loop deleted tenecin 1, reduced tenecin 1
     and tenecin 1 were chemical synthesized and their activities were measured.
     N-terminal loop deleted tenecin and reduced tenecin 1 did not show
     antibacterial activity.  CD spectroscopy data revealed that the
     α-helical content of tenecin 1 and the other proteins increased in
     the presence of 50% (volume/volume) trifluoroethanol (TFE) and the
     α-helical content of tenecin 1 was much higher than that of the
     other proteins in buffer with or without 50% (volume/volume) TFE.  These
     results suggest that disulfide bridges are necessary for the activity
     structure and the N-terminal loop plays an important role in the increase
     of α-helix in the membrane mimetic environment and the activity.
IT   220132-98-9
     RL: BAC (Biological activity or effector, except adverse); BSU (Biological
     study, unclassified); PRP (Properties); BIOL (Biological study)
        (structure-function study of tenecin 1 of Tenebrio molitor)
RN   220132-98-9  HCAPLUS
CN   L-Arginine, L-α-aspartyl-L-alanyl-L-alanyl-L-cysteinyl-L-alanyl-L-
     alanyl-L-histidyl-L-cysteinyl-L-leucyl-L-phenylalanyl-L-arginylglycyl-L-
```

arginyl-L-serylglycylglycyl-L-tyrosyl-L-cysteinyl-L-asparaginylglycyl-L-lysyl-L-arginyl-L-valyl-L-cysteinyl-L-valyl-L-cysteinyl-, cyclic (4→24),(8→26)-bis(disulfide), (18→3')-disulfide with L-valyl-L-threonyl-L-cysteine (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
REFERENCE COUNT: 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 2 OF 4 HCAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 1997:165206 HCAPLUS
DOCUMENT NUMBER: 126:154428
TITLE: Process for the identification of proteolytic activities and/or inhibitors thereof
INVENTOR(S): Fassina, Giorgio; Corti, Angelo
PATENT ASSIGNEE(S): Tecnogen S.C.P.A., Italy
SOURCE: Eur. Pat. Appl., 20 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 751225	A1	19970102	EP 1996-114931	19911014
EP 751225	B1	20010328		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE				
EP 481930	A2	19920422	EP 1991-830428	19911014
EP 481930	A3	19930630		
EP 481930	B1	19970618		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE				
AT 154609	E	19970715	AT 1991-830428	19911014
AT 200107	E	20010415	AT 1996-114931	19911014
PRIORITY APPLN. INFO.:			IT 1990-48365 A	19901015
			IT 1991-RM261 A	19910415
			EP 1991-830428 A3	19911014
			IT 1991-RO261	19910415

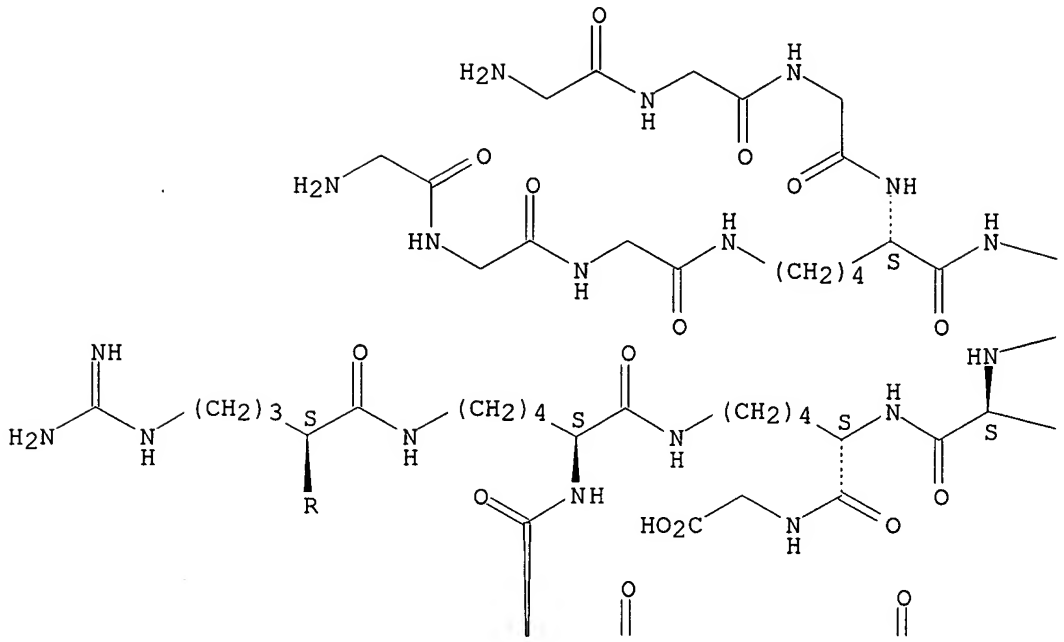
AB This invention relates to a process for the identification of proteolytic activities or of activities that inhibit proteolytic activities, particularly of endothelin and/or of TNF, especially in biol. fluids, fermentation broths, conditioned culture soils, cell exts., and plant exts. As an example, the process can use a fragment of proendothelin as substrate as well as a ligand comprising amino acid sequences that are hydropathically complementary to the fragment of proendothelin.

IT 143226-64-6
RL: RCT (Reactant); RACT (Reactant or reagent)
(determination of proendothelin- and TNF-specific proteolytic activities and their inhibitors)

RN 143226-64-6 HCAPLUS
CN Glycine, N2,N6-bis[N2,N6-bis[N2,N6-bis(glycylglycylglycyl)-L-lysyl-L-arginyl]-L-lysyl]-L-lysyl- (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



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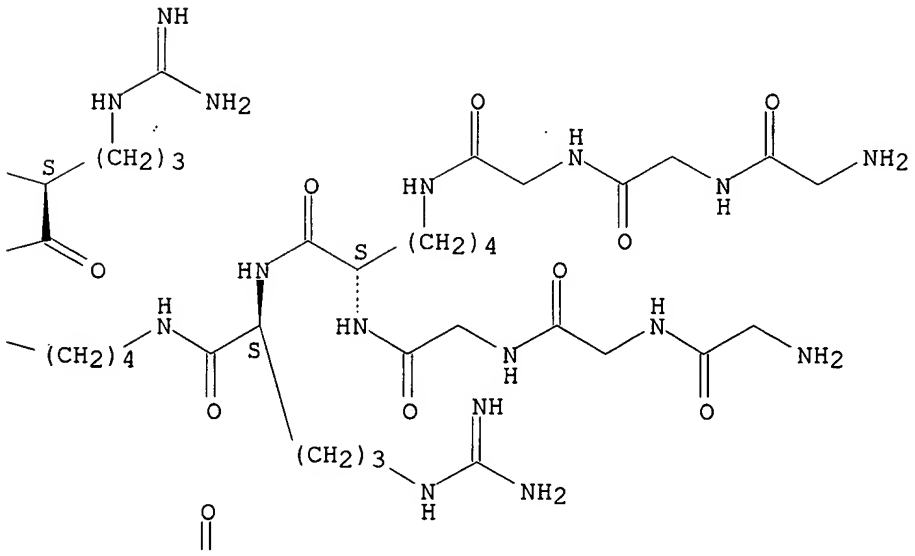

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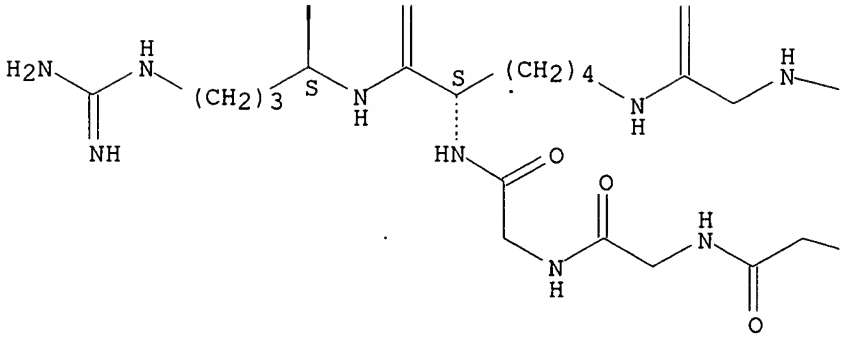

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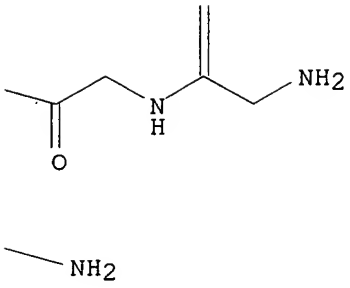

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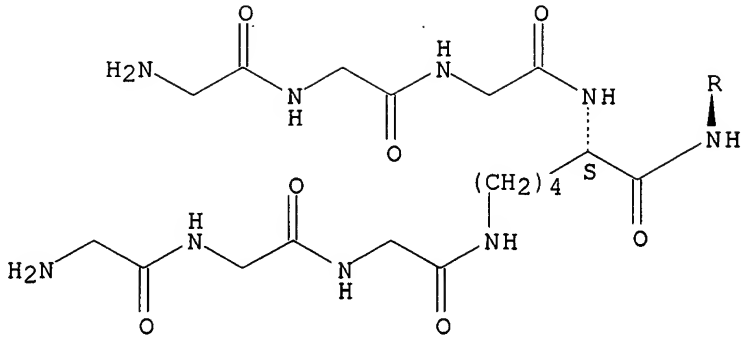


L4 ANSWER 3 OF 4 HCAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 1992:531566 HCAPLUS
DOCUMENT NUMBER: 117:131566
TITLE: Preparation of nonlinear peptides and their affinity for pro-endothelin and α-TNF fragments.
INVENTOR(S): Fassina Giorgio; Corti, Angelo
PATENT ASSIGNEE(S): Tecnogen S.C.P.A., Italy
SOURCE: Eur. Pat. Appl., 22 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent

LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 481930	A2	19920422	EP 1991-830428	19911014
EP 481930	A3	19930630		
EP 481930	B1	19970618		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE				
EP 751225	A1	19970102	EP 1996-114931	19911014
EP 751225	B1	20010328		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE				

PRIORITY APPLN. INFO.:

IT 1990-48365	A	19901015
IT 1991-RO261		19910415
IT 1991-RM261	A	19910415
EP 1991-830428	A3	19911014

AB Nonlinear peptides hydropathically complementary to peptides or protein portion with known amino acid sequence, e.g., pro-endothelin or α-TNF fragments, are prepared The above peptides comprise (1) an amino acid nucleus comprising at least an amino acid with at least 2 terminal amino functions and (2) a linear amino acid sequence which is hydropathically complementary to said known amino acid sequence and is bonded through a carbamido link to each one of said terminal amino functions. E.g., (K2K)2K-G, prepared from resin-bound α-,ε-bis(fluorenylmethoxycarbonyl)lysine and resin-bound Fmoc-Gly-OH, was condensed with RKFLAGLRARRLKF (Q) [also called ΔET(16-29), the polypeptide hydropathically complementary to the sequence 16-29 of the human Big Endothelin [1-38] (synthesized earlier)] to give [(Q2K)2]2-K-G [also called 8ΔET(16-29)]. The affinity of ET(16-29) for immobilized 8ΔET(16-29)] was about twice as that for immobilize ΔET(16-29).

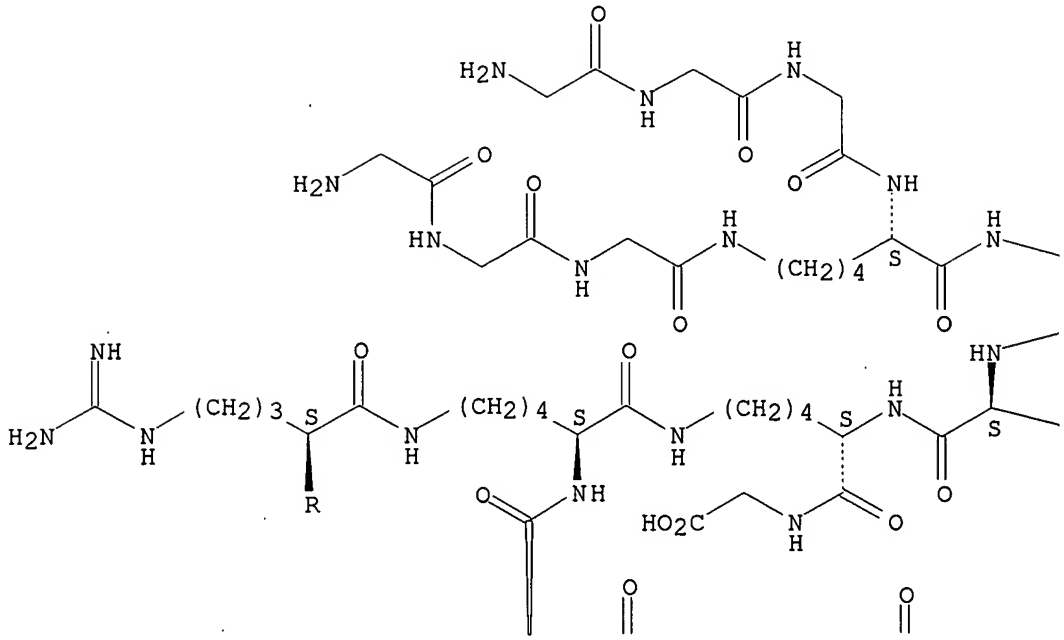
IT 143226-64-6P
RL: SPN (Synthetic preparation); PREP (Preparation)
(preparation of, for condensation with α-TNF fragment)

RN 143226-64-6 HCAPLUS

CN Glycine, N2,N6-bis[N2,N6-bis[N2,N6-bis(glycylglycylglycyl)-L-lysyl-L-arginyl]-L-lysyl]-L-lysyl- (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



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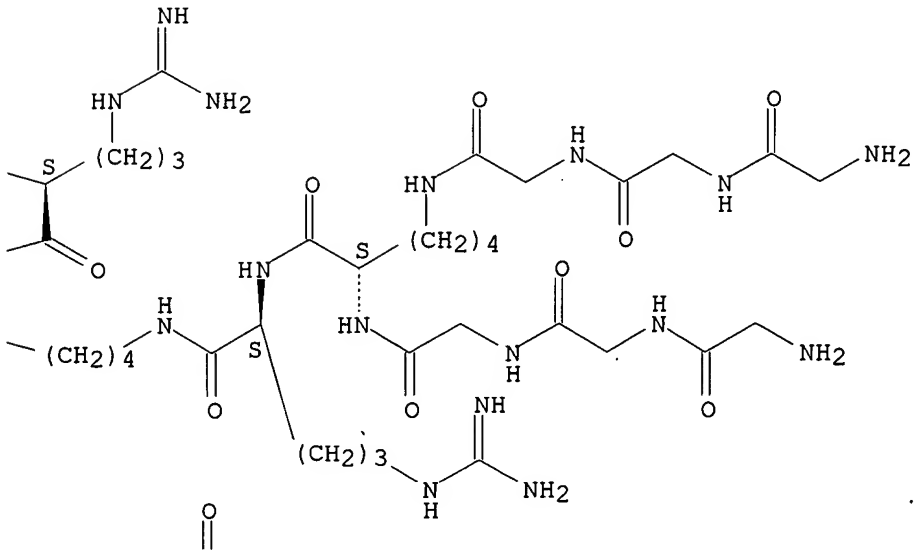

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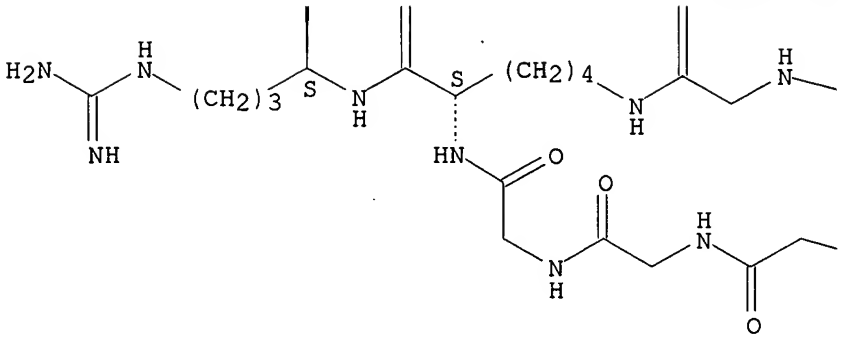

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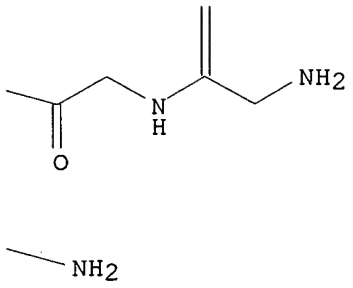

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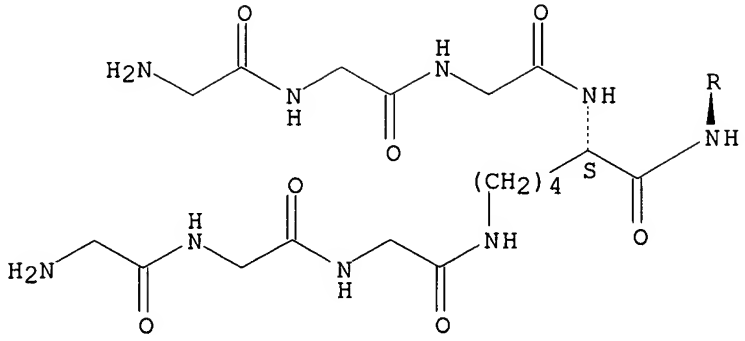


L4 ANSWER 4 OF 4 HCAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 1976:117721 HCAPLUS

DOCUMENT NUMBER: 84:117721

TITLE: Enzymic and immunochemical properties of lysozyme. XIII. Accurate delineation of the reactive site around the disulfide 6-127 by immunochemical study of β-propiolactone lysozyme derivative and of synthetic disulfide peptides

AUTHOR(S): Atassi, M. Z.; Koketsu, J.; Habeeb, A. F. S. A.

CORPORATE SOURCE: Dep. Chem., Wayne State Univ., Detroit, MI, USA

SOURCE: Biochimica et Biophysica Acta, Protein Structure (1976), 420(2), 358-75
CODEN: BBPTBH; ISSN: 0005-2795
DOCUMENT TYPE: Journal
LANGUAGE: English

AB In previous reports from this laboratory it was shown that an antigenic reactive site resides around the sequences 6-13 and 126-128 linked by the disulfide 6-127. The present work provides a strong support for the location of the reactive site by an independent approach. It also dets. accurately the boundaries of the reactive site. The 2 methionine residues in lysozyme were carboxyethylated by reaction with β-propiolactone. The electrophoretically homogeneous derivative had no other modified amino acids and showed no conformational changes, relative to native lysozyme, as determined by ORD and CD measurements. However, it exhibited a slight increase in disulfide reducibility relative to native lysozyme and its lytic activity was .apprx. half that of native lysozyme, probably as a result of the slight conformational change. On the other hand, the antigenic reactivity of the derivative was equal to that of native lysozyme with several goat and rabbit antisera to lysozyme. It was therefore concluded that methionines 12 and 105 were not parts of antigenic reactive sites in native lysozyme. Eleven peptides, corresponding to various sequences on the 2 sides of the disulfide 6-127 (i.e., 2 groups of peptides) were synthesized, purified, and characterized. One group (A) of peptides comprised sequences 3-14, 5-14, 6-14, 5-13, 5-12, and an analog of sequence 5-14 in which methionine 12 was replaced by glycine. The 2nd group (B) of peptides comprised sequences 125-129, 125-128, 126-128, 127-128, and 125-127. From groups A and B, 9 disulfide-containing peptides were synthesized, purified, and characterized and their immunochem. interactions with antisera to native lysozyme studied. Towards each of the antisera studied here, Phe-3, Gly-4, Arg-5, Arg-125, and Leu-129 were not essential parts of the reactive site. On the other hand, Arg-14, Lys-13, Gly-126, and with some antisera Arg-128 were each critical for the reactivity of the site. Peptides from group A alone or group B alone did not inhibit the reaction of lysozyme with its antisera, confirming the previous findings that the integrity of the disulfide bond is essential for bringing the 2 distant (in sequence) parts of the site together. Finally, replacement of Met-12 by glycine did not influence the immunochem. reactivity of the site, confirming the above conclusion that neither of the 2 methionine residues takes part in interaction of lysozyme with its antibodies. An accurate delineation of the antigenic reactive site is, therefore derived here and its shape in the 3-dimensional structure of native lysozyme is described.

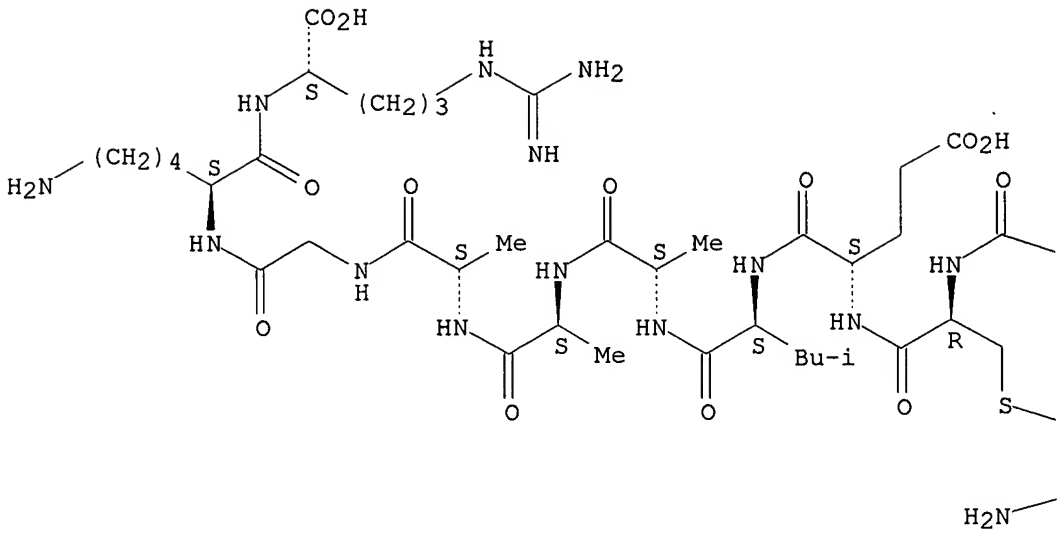
IT 58635-06-6P
RL: SPN (Synthetic preparation); PREP (Preparation)
(preparation of and lysozyme antisera response to)

RN 58635-06-6 HCAPLUS

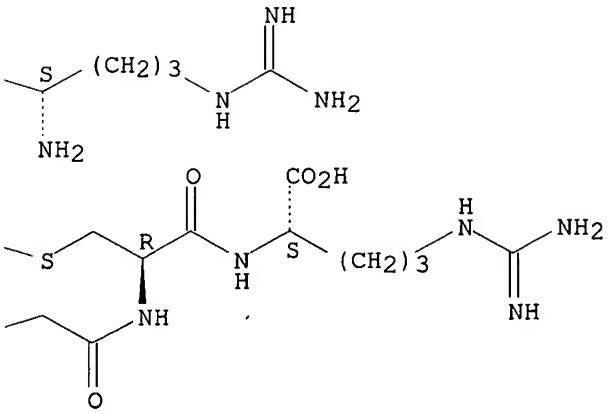
CN L-Arginine, L-arginyl-L-cysteinyl-L-α-glutamyl-L-leucyl-L-alanyl-L-alanyl-L-alanylglycyl-L-lysyl-, (2→2')-disulfide with glycyl-L-cysteinyl-L-arginine (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B



=> fil reg

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DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION

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=> s LIGK/SQSP
L5       22902 LIGK/SQSP

=> L5 and PAR
          7199 PAR
            19 PARS
          7218 PAR
                 (PAR OR PARS)
L6           8 L5 AND PAR

=> fil hcap uspatful
COST IN U.S. DOLLARS                            SINCE FILE      TOTAL
                                                   ENTRY    SESSION
FULL ESTIMATED COST                                33.65      70.80

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)      SINCE FILE      TOTAL
                                                   ENTRY    SESSION
CA SUBSCRIBER PRICE                                 0.00      -3.00

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=> L6
L7           10 L6

=> d L7 1-10 ibib abs hitstr
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L7 ANSWER 1 OF 10 HCAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2006:239773 HCAPLUS
DOCUMENT NUMBER: 144:409183
TITLE: Jab1, a Novel Protease-activated Receptor-2 (PAR-2)-interacting Protein, Is Involved in PAR-2-induced Activation of Activator Protein-1
AUTHOR(S): Luo, Weibo; Wang, Yingfei; Hanck, Theodor; Stricker, Rolf; Reiser, Georg
CORPORATE SOURCE: Institut fuer Neurobiochemie, Medizinische Fakultaet, Otto-von-Guericke-Universitaet Magdeburg, Magdeburg, 39120, Germany
SOURCE: Journal of Biological Chemistry (2006), 281(12), 7927-7936
CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Protease-activated receptor-2 (PAR-2), a G protein-coupled receptor for trypsin and tryptase, exerts important physiol. and pathol. functions in multiple systems. However, unlike PAR-1, the PAR-2-mediated intracellular signal transductions are hardly known. Here, using yeast two-hybrid screening with a human brain cDNA library, we identified an interacting partner of human PAR-2, the Jun activation domain-binding protein 1 (Jab1). The interaction was confirmed by glutathione S-transferase pull-down assays in vitro, and by co-immunopptn. assays in vivo. Jab1 was also shown to be colocalized with PAR-2 in both transfected HEK293 cells and in normal primary human astrocytes by double immunofluorescence staining. Further expts. demonstrated that multiple intracellular domains of PAR-2 are required for the interaction with Jab1. We then showed that agonist stimulation of PAR-2 disrupted the interaction, which could be prevented by the inhibitor of receptor endocytosis phenylarsine oxide, but not by the lysosomal protease inhibitor ZPAD. Importantly, we found that activation of PAR-2 induced the redistribution of Jab1 from the plasma membrane to the cytosol, but did not influence expression of Jab1. Furthermore, Jab1 mediated PAR-2-induced c-Jun activation, which was followed by increased activation of activator protein-1. Loss-of-function studies, using Jab1 small interfering RNA, demonstrated that Jab1 knockdown blocked PAR-2-induced activator protein-1 activation. Taken together, our data demonstrate that Jab1 is an important effector that mediates a novel signal transduction pathway for PAR-2-dependent gene expression.

IT 557050-32-5
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; sequence of human proteinase-activated receptor PAR-2)
RN 557050-32-5 HCAPLUS
CN Proteinase-activated receptor PAR-2 (human cell line HEK293; A549 gene F2RL1) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
REFERENCE COUNT: 50 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 2 OF 10 HCAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2005:1120863 HCAPLUS

DOCUMENT NUMBER: 143:340424
TITLE: Coping with cold: The genome of the versatile marine Antarctica bacterium Pseudoalteromonas haloplanktis TAC125
AUTHOR(S): Medigue, Claudine; Krin, Evelyne; Pascal, Geraldine; Barbe, Valerie; Bernsel, Andreas; Bertin, Philippe N.; Cheung, Frankie; Cruveiller, Stephane; D'Amico, Salvino; Duilio, Angela; Fang, Gang; Feller, Georges; Ho, Christine; Mangenot, Sophie; Marino, Gennaro; Nilsson, Johan; Parrilli, Ermenegilda; Rocha, Eduardo P. C.; Rouy, Zoe; Sekowska, Agnieszka; Tutino, Maria Luisa; Vallenet, David; von Heijne, Gunnar; Danchin, Antoine
CORPORATE SOURCE: Genoscope, CNRS-UMR 8030, Atelier de Genomique Comparative, Evry, 91006, Fr.
SOURCE: Genome Research (2005), 15(10), 1325-1335
CODEN: GEREFS; ISSN: 1088-9051
PUBLISHER: Cold Spring Harbor Laboratory Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A considerable fraction of life develops in the sea at temps. lower than 15°. Little is known about the adaptive features selected under those conditions. The genome of the fast growing Antarctica bacterium Pseudoalteromonas haloplanktis TAC125 was sequenced and analyzed. The bacterium copes with the increased solubility of oxygen at low temperature by multiplying O2 scavenging while deleting whole pathways producing reactive oxygen species. O2-consuming lipid desaturases achieve both protection against oxygen and synthesis of lipids making the membrane fluid. A remarkable strategy for avoidance of reactive oxygen species generation is developed by P. haloplanktis, with elimination of the ubiquitous molybdopterin-dependent metabolism The P. haloplanktis proteome reveals a concerted amino acid usage bias specific to psychrophiles, consistently appearing apt to accommodate asparagine, a residue prone to make proteins age. Adding to its originality, P. haloplanktis further differs from its marine counterparts with recruitment of a plasmid origin of replication for its second chromosome.

IT 865976-88-1
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence of the versatile marine Antarctica bacterium Pseudoalteromonas haloplanktis TAC125)
RN 865976-88-1 HCAPLUS
CN Paraquat-inducible protein B (Pseudoalteromonas haloplanktis strain TAC125 gene pqiB) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
REFERENCE COUNT: 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 3 OF 10 HCAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2005:379326 HCAPLUS
DOCUMENT NUMBER: 143:400611
TITLE: The genome sequence of Salmonella enterica serovar Choleraesuis. [Erratum to document cited in CA142:387014]
AUTHOR(S): Chiu, Cheng-Hsun; Tang, Petrus; Hu, Chishih ChuSongnian; Bao, Qiyu; Yu, Jun; Chou, yun-Ying; Wang, Hsin-Shih; Lee, Ying-Shiung

CORPORATE SOURCE: Department of Pediatrics, Chang Gung Children's Hospital, Taoyuan, Taiwan
SOURCE: Nucleic Acids Research (2005), 33(7), 2351
CODEN: NARHAD; ISSN: 0305-1048
PUBLISHER: Oxford University Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The correct version of Figure 3B is given. In Materials and Methods, between the paragraphs "Electron microscopy" and "Inhibition assay and western blot analysis" the following paragraph should be inserted:. "Chemotaxis of S. Choleraesuis SC-B67 and S. Typhimurium LT2 towards chemotactic attractants, glucose and pyrroloquinolone quinone (PQQ), was investigated by using the tube swarming assay (20, 21). The agar tube consisted of two layers: both upper and lower layers contained tryptone (10 g/l), NaCl (5 gl), and 2,3,5-triphenyltetrazolium chloride (0.05 g/l) in an agar base, while only the lower layer was added with either glucose (1 mM) and/or PQQ (10 (M)). The 2,3,5-triphenyltetrazolium chloride (0.05 g/l) acts as a color indicator when bacteria grew and moved. For each test, approx. 3 x 106 CFU of bacteria, pre-grown to late log phase, were transferred to the top of the agar tube. The tube was then incubated at 37°C and the swarming length of the bacteria (red area) was measured every hour.".
IT 849871-00-7
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genome sequence of Salmonella enterica serovar Choleraesuis (Erratum))
RN 849871-00-7 HCAPLUS
CN Paral rRNA methyltransferase (Salmonella enterica enterica choleraesuis strain SC-B67 gene yebU) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L7 ANSWER 4 OF 10 HCAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2005:291212 HCAPLUS
DOCUMENT NUMBER: 142:387014
TITLE: The genome sequence of Salmonella enterica serovar Choleraesuis
AUTHOR(S): Chiu, Cheng-Hsun; Tang, Petrus; Chu, Chishih; Hu, Songnian; Bao, Qiyu; Yu, Jun; Chou, Yun-Ying; Wang, Hsin-Shih; Lee, Ying-Shiung
CORPORATE SOURCE: Department of Pediatrics, Chang Gung Children's Hospital, Taoyuan, Taiwan
SOURCE: Nucleic Acids Research (2005), 33(5), 1690-1698
CODEN: NARHAD; ISSN: 0305-1048
PUBLISHER: Oxford University Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Salmonella enterica serovar Choleraesuis (S. choleraesuis), a highly invasive serovar among non-typhoidal Salmonella, usually causes sepsis or extra-intestinal focal infections in humans. S. choleraesuis infections have now become particularly difficult to treat because of the emergence of resistance to multiple antimicrobial agents. The 4.7-Mb genome sequence of a multidrug-resistant S. choleraesuis strain SC-B67 was determined Genome-wide comparison of 3 sequenced Salmonella genomes revealed that more deletion events occurred in S. choleraesuis SC-B67 and S. typhi CT18 relative to S. typhimurium LT2. S. choleraesuis has 151 pseudogenes, which, among the 3 Salmonella genomes, include the highest percentage of

pseudogenes arising from the genes involved in bacterial chemotaxis signal-transduction pathways. Mutations in these genes may increase smooth swimming of the bacteria, potentially allowing more effective interactions with and invasion of host cells to occur. A key regulatory gene of TetR/AcrR family, acrR, was inactivated through the introduction of an internal stop codon resulting in overexpression of AcrAB that appears to be associated with ciprofloxacin resistance. While lateral gene transfer providing basic functions to allow niche expansion in the host and environment is maintained during the evolution of different serovars of Salmonella, genes providing little overall selective benefit may be lost rapidly. These findings suggest that the formation of pseudogenes may provide a simple evolutionary pathway that complements gene acquisition to enhance virulence and antimicrobial resistance in S. choleraesuis. The genome sequence is deposited in GenBank/EMBL/DDBJ under accession nos. AE017220 (chromosome), AY509003 (plasmid pSCV50), and AY509004 (plasmid pS138).

IT 849871-00-7
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genome sequence of Salmonella enterica serovar Choleraesuis)

RN 849871-00-7 HCAPLUS

CN Paral rRNA methyltransferase (Salmonella enterica enterica choleraesuis strain SC-B67 gene yebU) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

REFERENCE COUNT: 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 5 OF 10 HCAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2005:176846 HCAPLUS

DOCUMENT NUMBER: 142:234200

TITLE: Life at depth: Photobacterium profundum genome sequence and expression analysis

AUTHOR(S): Vezzi, A.; Campanaro, S.; D'Angelo, M.; Simonato, F.; Vitulo, N.; Lauro, F. M.; Cestaro, A.; Malacrida, G.; Simionati, B.; Cannata, N.; Romualdi, C.; Bartlett, D. H.; Valle, G.

CORPORATE SOURCE: CRIBI Biotechnology Centre and Department of Biology, Universita di Padova, Padua, 35131, Italy

SOURCE: Science (Washington, DC, United States) (2005), 307(5714), 1459-1461
CODEN: SCIEAS; ISSN: 0036-8075

PUBLISHER: American Association for the Advancement of Science

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Deep-sea life requires adaptation to high pressure, an extreme yet common condition given that oceans cover 70% of Earth's surface and have an average depth of 3800 m. Survival at such depths requires specific adaptation but, compared with other extreme conditions, high pressure has received little attention. Recently, Photobacterium profundum strain SS9 has been adopted as a model for piezophily. This report describes its genome sequence (6.4 megabase pairs) and transcriptome anal. The results provide a first glimpse into the mol. basis for life in the largest portion of the biosphere, revealing high metabolic versatility. The tripartite genome sequence for the 4.1-Mbp major chromosome 1, 2.2-Mbp minor chromosome 2, and plasmid are deposited in GenBank/EMBL/DDBJ under accession nos. CR354531, CR354532, and CR377818, resp.

IT 679348-83-5
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; Photobacterium profundum genome sequence and expression anal.)
RN 679348-83-5 HCAPLUS
CN Uncharacterized paraquat-inducible protein B (Photobacterium profundum strain SS9 gene XCC0115) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
REFERENCE COUNT: 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 6 OF 10 HCAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2004:775882 HCAPLUS
DOCUMENT NUMBER: 141:288987
TITLE: Diagnostics, drug screening and therapeutics for diseases associated with human G-protein coupled proteinase activated receptor 2 (PAR-2)
INVENTOR(S): Golz, Stefan; Brueggemeier, Ulf; Summer, Holger
PATENT ASSIGNEE(S): Bayer Healthcare A.-G., Germany
SOURCE: PCT Int. Appl., 121 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004080373	A2	20040923	WO 2004-EP1896	20040226
WO 2004080373	A3	20050623		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
EP 1604207	A2	20051214	EP 2004-714741	20040226
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK				

PRIORITY APPLN. INFO.: EP 2003-4980 A 20030311
WO 2004-EP1896 W 20040226

AB The invention provides a human PAR-2 which is associated with the cardiovascular disorders, gastrointestinal and liver diseases, hematol. disorders, respiratory diseases, neurol. disorders and urol. disorders. The invention is based on an expression profile for PAR-2 mRNA distribution in human cells and tissues as determined by PCR. Thus, the invention provides assays for the identification of compds. useful in the treatment or prevention of these disorders and diseases (no data). The invention also features compds. (no data) which bind to and/or activate or inhibit the activity of PAR-2 as well as pharmaceutical compns. comprising such compds.
IT 761570-28-9

RL: ANT (Analyte); BSU (Biological study, unclassified); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(amino acid sequence; diagnostics, drug screening and therapeutics for diseases associated with human G-protein coupled proteinase activated receptor 2 (PAR-2))
RN 761570-28-9 HCAPLUS
CN Receptor PAR-2 (proteinase-activated receptor 2) (human) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L7 ANSWER 7 OF 10 HCAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2001:818860 HCAPLUS
DOCUMENT NUMBER: 136:80679
TITLE: Complete genome sequence of Salmonella enterica serovar typhimurium LT2
AUTHOR(S): McClelland, Michael; Sanderson, Kenneth E.; Spleth, John; Clifton, Sandra W.; Latreille, Phil; Courtley, Laura; Porwolilk, Steffen; All, Johar; Daute, Mike; Du, Felyu; Hou, Shunfang; Layman, Dan; Leonard, Shawn; Nguyen, Christine; Scott, Kelsi; Holmes, Andrea; Grewal, Neenu; Mulvaney, Elizabeth; Ryan, Ellen; Sun, Hul; Florea, Lillana; Miller, Webb; Stoneking, Tamberiyn; Nhan, Michael; Waterston, Robert; Wilson, Richard K.
CORPORATE SOURCE: Sidney Kimmel Cancer Center, San Diego, CA, 92121, USA
SOURCE: Nature (London, United Kingdom) (2001), 413(6858), 852-856
CODEN: NATUAS; ISSN: 0028-0836
PUBLISHER: Nature Publishing Group
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Salmonella enterica subspecies I, serovar typhimurium (S. typhimurium), is a leading cause of human gastroenteritis, and is used as a mouse model of human typhoid fever. The incidence of non-typhoid salmonellosis is increasing worldwide, causing millions of infections and many deaths in the human population each year. The 4857-kilobase (kb) chromosome and 94-kb virulence plasmid of S. typhimurium strain LT2 has now been sequenced.. The distribution of close homologs of S. typhimurium LT2 genes in 8 related enterobacteria was determined using previously completed genomes of 3 related bacteria, sample sequencing of both S. enterica serovar paratyphi A (S. paratyphi A) and Klebsiella pneumoniae, and hybridization of 3 unsequenced genomes to a microarray of S. typhimurium LT2 genes. Lateral transfer of genes is frequent, with 11% of the S. typhimurium LT2 genes missing from S. enterica serovar Typhi (S. typhi), and 29% missing from Escherichia coli K12. The 352 gene homologs of S. typhimurium LT2 confined to subspecies I of S. enterica - containing most mammalian and bird pathogens - are useful for studies of epidemiol., host specificity, and pathogenesis. Most of these homologs were previously unknown, and 50 may be exported to the periplasm or outer membrane, rendering them accessible as therapeutic or vaccine targets. The sequences are available from the GenBank database under Accession Nos. AE006468 (chromosome) and AE006471 (pSTL).
IT 384927-61-1
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(amino acid sequence; complete genome sequence of Salmonella enterica serovar typhimurium LT2)
RN 384927-61-1 HCAPLUS
CN Paral rRNA methyltransferase (Salmonella enterica typhimurium strain LT2; SGSC 1412; ATCC 700720 gene yebU) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
REFERENCE COUNT: 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 8 OF 10 HCAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2000:756854 HCAPLUS
DOCUMENT NUMBER: 133:318302
TITLE: Protein and cDNA sequences of human protease activated receptor 2 (PAR-2) polymorphic variants and diagnostic and therapeutic uses thereof
INVENTOR(S): Walls, Andrew Finlay; Palmer, Karen-Jane; Compton, Steven John; Cairns, Jennifer Ann; Gough, Alan Charles
PATENT ASSIGNEE(S): University of Southampton, UK
SOURCE: PCT Int. Appl., 59 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000063371	A1	20001026	WO 2000-GB1455	20000417
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2370272	AA	20001026	CA 2000-2370272	20000417
EP 1165790	A1	20020102	EP 2000-927405	20000417
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
JP 2002541843	T2	20021210	JP 2000-612450	20000417
PRIORITY APPLN. INFO.:			GB 1999-8513 A	19990415
			WO 2000-GB1455 W	20000417

AB The invention provides protein and cDNA sequences of human protease activated receptor 2 (PAR-2) polymorphic variants which are believed to be a new G-protein regulated receptor. A PAR-2 polymorphic variant or a fragment thereof is provided which (i) has reduced sensitivity to trypsin as compared with wild type PAR-2; (ii) has increased sensitivity to trans-cinnamoyl-LIGRLO-NH2 as compared with wild type PAR-2; and (iii) is activated by TLIGRL-NH2, which polypeptide or fragment thereof comprises an extracellular loop 2 (ECL-2) having at least one amino acid difference from the corresponding ECL-2 amino acid sequence of the wild type polypeptide.
IT 172143-36-1P
RL: BAC (Biological activity or effector, except adverse); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP

(Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; protein and cDNA sequences of human protease activated receptor 2 (PAR-2) polymorphic variants and diagnostic and therapeutic uses thereof)
RN 172143-36-1 HCAPLUS
CN Receptor PAR 2 (human clone 1142 protein G-coupled proteinase-activated precursor reduced) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
REFERENCE COUNT: 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 9 OF 10 HCAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 1996:198071 HCAPLUS
DOCUMENT NUMBER: 124:253787
TITLE: Molecular cloning, expression and potential functions of the human proteinase-activated receptor-2
AUTHOR(S): Boehm, Stephan K.; Kong, Wuyi; Broemme, Dieter; Smeekens, Steven P.; Anderson, David C.; Connolly, Andrew; Kahn, Mark; Nelken, Nicholas; Coughlin, Shaun R.; et al.
CORPORATE SOURCE: Dep. Surg., Univ. California, San Francisco, CA, 94143-0660, USA
SOURCE: Biochemical Journal (1996), 314(3), 1009-16
CODEN: BIJOAK; ISSN: 0264-6021
PUBLISHER: Portland Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB We used PCR to amplify proteinase activated receptor-2 (PAR-2) from human kidney cDNA. The open reading frame comprised 1191 bp and encoded a protein of 397 residues with 83% identify with mouse PAR-2. In KNRK cells (a line of kirsten murine sarcoma virus-transformed rat kidney-epithelial cells) transfected with this cDNA, trypsin and activating peptide (AP) corresponding to the tethered ligand exposed by trypsin cleavage (SLIGKV-NH2) induced a prompt increase in cytosolic calcium ion concentration ([Ca2+]i). Human PAR-2 (hPAR-2) resided both on the plasma membrane and in the Golgi apparatus HPAR-2 mRNA was highly expressed in human pancreas, kidney, colon, liver and small intestine, and by A549 lung and SW480 colon adenocarcinoma cells. Hybridization in situ revealed high expression in intestinal epithelial cells throughout the gut. Trypsin and AP stimulated an increase in [Ca2+]i in a rat intestinal epithelial cell line (hBRIE 380) and stimulated amylase secretion in isolated pancreatic acini. In A549 cells, which also responded to trypsin and AP with mobilization of cytosolic Ca2+, AP inhibited colony formation. Thus PAR-2 may serve as a trypsin sensor in the gut. Its expression by cells and tissues not normally exposed to pancreatic trypsin suggests that other proteases could serve as physiol. activators.
IT 175389-69-2
RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(amino acid sequence; mol. cloning, expression and potential functions of the human proteinase-activated receptor-2)
RN 175389-69-2 HCAPLUS
CN Receptor PAR 2 (human kidney proteinase-activated precursor reduced) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L7 ANSWER 10 OF 10 HCAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 1995:786725 HCAPLUS
DOCUMENT NUMBER: 124:46907
TITLE: Molecular cloning and functional expression of the gene encoding the human proteinase-activated receptor 2
AUTHOR(S): Nystedt, Sverker; Emilsson, Kjell; Larsson, Anna-Karin; Stroembeck, Bodil; Sundelin, Johan
CORPORATE SOURCE: Wallenberg Laboratory, Lund Univ., Swed.
SOURCE: European Journal of Biochemistry (1995), 232(1), 84-9
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DOCUMENT TYPE: Journal
LANGUAGE: English

AB The cloning and functional expression of the gene encoding the human proteinase-activated receptor 2 is described. The gene is divided into 2 exons separated by about 14 kb intronic DNA. The deduced protein sequence is 397 amino acids long and 83% identical to the mouse receptor sequence. Within the extracellular amino terminus, the residues predicted to form the tethered agonist ligand differ between the 2 receptors; of the first 6 residues only 4 are conserved. At positions 5 and 6 a Lys residue and a Val residue, resp., have replaced Arg and Leu residues found in the mouse sequence. When the human receptor is expressed in Chinese hamster ovary cells, it can be activated by low nanomolar concns. of the Ser proteinase trypsin and by peptides made from the receptor sequence. Northern-blot anal. of receptor expression showed that the receptor transcript is widely expressed in human tissues with especially high levels in pancreas, liver, kidney, small intestine and colon. Moderate expression was detected in many organs but none in brain or skeletal muscle. By fluorescence in situ hybridization, the human proteinase-activated receptor 2 gene was mapped to chromosomal region 5q13, where, previously, the related thrombin receptor gene has been located.

IT 172143-36-1
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; cloning, sequence and functional expression of the gene encoding the human proteinase-activated receptor 2)

RN 172143-36-1 HCAPLUS
CN Receptor PAR 2 (human clone 1142 protein G-coupled proteinase-activated precursor reduced) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***